



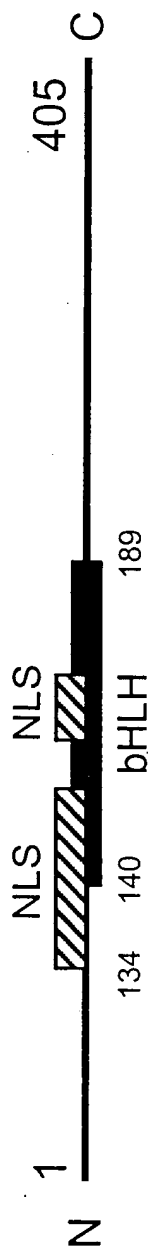
Title: PHELIX: A TESTIS-SPECIFIC PROTEIN EXPRESSED IN
CANCER

First Inventor: Daniel E. H. AFAR, *et al.*

Application No.: 09/389,000

Docket No.: 511582002700

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NLS = nuclear localization signals, residues 134-150, 163-169.
bHLH = basic helix-loop-helix domain, residues 140-189.

FIG. 1



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5' 11 20 29 38 47 56
GAC CGG GGG GCG GTT GGG GTT CAC CGC CTC GTG CCG TAC TGG CTT CTG GGT GGC

65 74 83 92 101 110
CCT TAA TGT CTT GTG CTC TAA GGT GCT GAG GGG AAA GAC GCG GGA GGT CTC TGG

119 128 137 146 155 164
CCT GAC ACT ATG AAG GAA GAG AGA AAC TAC AAC TTC GAC GGT GTG AGC ACC AAC

173 182 191 200 209 218
CGC CTG AAA CAG CAG TTG CTG GAA GAA GTC CGC AAG AAG TAG TGA ATG GAA AAC

227 236 245 254 263 272
CCG TTA TGA GAC ACA ACT TGA ATT AAA TGA TGA ACT AGA AAA GCA AAT TGT TTA

281 290 299 308 317 326
TCT CAA GGA GAA AGT GGA AAA AAT CCA TGG AAA CTC TTC AGA TAG ACT ATC TTC

335 344 353 362 371 380
TAT TCG TGT CTA TGA ACG AAT GCC AGT GGA ATC CTT AAA CAC ATT ACT TAA ACA

389 398 407 416 425 434
GCT AGA AGA AGA AAA GAA GAC TCT TGA AAG TCA AGT GAA ATA CTA TGC ACT TAA

443 452 461 470 479 488
ACT GGA ACA AGA ATC AAA GGC TTA CCA GAA GAT CAA CAA TGA ACG CCG TAC ATA

497 506 515 524 533 542
CCT AGC TGA AAT GTC TCA GGG TTC TGG TTT ACA TCA AGT TTC TAA AAG GCA ACA

551 560 569 578 587 596
GGT GGA TCA ACT GCC TAG GAT GCA AGA GAA TCT AGT GAA AAC GCA AAA ATA GAC

605 614 623 632 641 650
ATC TTA TTA GTT GGA GAT GTC ACT GTG GGC TAC CTG GCT GAT ACT GTA CAG AAA

659 668 677 686 695 704
CTA TTT GCA AAC ATA GCA GAA GTC ACC ATC ACC ATC AGT GAC ACG AAG GAG GCA

713 722 731 740 749 758
GCA GCG CTT TTG GAT GAT TGC ATA TTC AAC ATG GTT CTC TTG AAG GTG CCT TCT

M V L L K V P S

767 776 785 794 803 812
TCA CTA AGT GCC GAG GAG CTG GAA GCC ATC AAG TTA ATT AGA TTT GGC AAA AAG

S L S A E E L E A I K L I R F G K K

821 830 839 848 857 866
AAA AAT ACA CAT TCA CTG TTT GTT TTT ATA ATC CCT GAA AAT TTT AAA GGT TGT

K N T H S L F V F I I P E N F K G C

875 884 893 902 911 920
ATT TCA GGG CAT GGA ATG GAT ATT GCT TTA ACT GAA CCA CTG ACA ATG GAA AAA

I S G H G M D I A L T E P L T M E K

929 938 947 956 965 974
ATG AGT AAT GTG GTA AAA TAC TGG ACA ACA TGT CCC TCA AAC ACT GTT AAG ACT

M S N V V K Y W T T C P S N T V K T

FIG. 2A



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983 992 1001 1010 1019 1028
GAA AAC GCA ACT GGG CCT GAA GAA CTT GGA TTG CCC CTG CAG AGG TCC TAC AGC
E N A T G P E E L G L P L Q R S Y S

1037 1046 1055 1064 1073 1082
GAA CAC CTG GGA TAT TTT CCT ACT GAT CTA TTT GCC TGC TCT GAA TCT TTA AGG
E H L G Y F P T D L F A C S E S L R

1091 1100 1109 1118 1127 1136
AAT GGC AAT GGG CTT GAA TTA AAT GCT TCG TTG TCA GAG TTC GAG AAA AAC AAA
N G N G L E L N A S L S E F E K N K

1145 1154 1163 1172 1181 1190
AAG ATC TCT CTT CTT CAT TCA AGC AAG GAA AAA CTA AGA AGG GAA AGA ATC AAA
K I S L L H S S K E K L R R E R I K

1199 1208 1217 1226 1235 1244
TAT TGC TGT GAG CAG CTG CGT ACT CTC TTG CCG TAT GTA AAA GGG AGA AAG AAT
Y C C E Q L R T L L F Y V K G R K N

1253 1262 1271 1280 1289 1298
GAT GCG GCT TCA GTT CTT GAG GCA ACA GTT GAT TAT GTG AAA TAT ATC CGG GAG
D A A S V L E A T V D Y V K Y I R E

1307 1316 1325 1334 1343 1352
AAA ATC TCT CCA GCC GTT ATG GCC CAG ATT ACA GAA GCA CTT CAG AGC AAC ATG
K I S P A V M A Q I T E A L Q S N M

1361 1370 1379 1388 1397 1406
AGG TTT TGT AAG AAA CAA CAA ACA CCC ATT GAG CTG TCT CTC CCA GGC ACT GTC
R F C K K Q Q T P I E L S L P G T V

1415 1424 1433 1442 1451 1460
ATG GCA CAG CGG GAA AAC AGT GTG ATG AGC ACT TAC TCC CCT GAG AGA GGG CTC
M A Q R E N S V M S T Y S P E R G L

1469 1478 1487 1496 1505 1514
CAA TTC CTG ACT AAT ACG TGC TGG AAT GGG TGC TCC ACT CCT GAT GCA GAG AGC
Q F L T N T C W N G C S T P D A E S

1523 1532 1541 1550 1559 1568
TCC TTG GAT GAA GCT GTG AGA GTT CCA TCA AGC TCC GCC TCA GAG AAT GCT ATT
S L D E A V R V P S S S A S E N A I

1577 1586 1595 1604 1613 1622
GGT GAT CCA TAT AAA ACT CAC ATT TCC AGT GCA GCG CTG TCT CTG AAT TCC TTG
G D P Y K T H I S S A A L S L N S L

1631 1640 1649 1658 1667 1676
CAT ACT GTC AGA TAT TAT TCT AAA GTC ACC CCT TCC TAC GAT GCA ACT GCT GTA
H T V R Y Y S K V T P S Y D A T A V

FIG. 2B



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1685	1694	1703	1712	1721	1730
ACA AAT CAG AAC ATT TCA ATT CAT TTA CCT TCA GCC ATG CCC CCG GTC TCA AGC					
T N Q N I S I H L P S A M P P V S S					
1739	1748	1757	1766	1775	1784
TTC TCC CTC GGC ACT GCA CTT CTG GGT TGG GCC AGA CGT GCA CTA CAC ATC CCA					
F S L G T A L L G W A R R A L H I P					
1793	1802	1811	1820	1829	1838
ACT GTC TGC AAC AGT TTT GGG CGT ATT AAA AGC ACA TGT TTG AAA TTC ACA CTC					
T V C N S F G R I K S T C L K F T L					
1847	1856	1865	1874	1883	1892
TCA ACC ACC TAC TGG GCG CAG TTT GAC AAT CTA GGA AAA GTG GAA CAA AGA ATG					
S T T Y W A Q F D N L G K V E Q R M					
1901	1910	1919	1928	1937	1946
ATT TTG AAA GCT CCA CCC AAA GAC CTA ATA TCA AAA GAG TTG GCA TGG TTT GGC					
I L K A P P K D L I S K E L A W F G					
1955	1964	1973	1982	1991	2000
TTC TGA TAA ATG CAC TCA AAG CTT CTG CAG ATA GAA AGA CCA GCA GCG AAA AAG					
F * *					
2009	2018	2027	2036	2045	2054
CTG GCC ACA CAC TGT CAC TCA TCT TCA TAC ACA CTT GGA TCC CCG CCA GCC AGA					
2063	2072	2081	2090	2099	2108
GAG CTA CAA GAA CAA ATG GCC TCA GTG ACC TAC ACT CTC TTT TCT CAA AAA ATA					
2117	2126				
TTC CAC AAT TTA TGA AAA AAA A 3'					

FIG. 2C



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Homology with Max (rat)

gnl|PID|d1003848 (D14448) Max [Rattus norvegicus]
Length = 151

Score = 93 (42.1 bits), Expect = 0.00037, P = 0.00037
Identities = 17/50 (34%), Positives = 30/50 (60%)

22P4G9: 5 HSSKEKLRRLRIKYCCEQLRTLLPYVKGRKNDAAVLEATVDYVKYIREK 54
H++ E+ RR+ IK LR +P ++G K A +L+ +Y++Y+R K
Max: 19 HNALERKRRDHIKDSFHSRLRDSVPSLQGEKASRAQILDKATEYIQYMRRK 68

Homology with Mxi (zebrafish)

sp|P50541|MXI1_BRARE MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN)
gi|505977
(U10638) zMxi1 [Brachydanio rerio]
Length = 243

Score = 64 (29.0 bits), Expect = 3.3, P = 0.96
Identities = 11/24 (45%), Positives = 17/24 (70%)

22P4G9: 5 HSSKEKLRRLRIKYCCEQLRTLLP 28
H+ EK RR ++ C E+L+TL+P
Mxi: 81 HNELEKNRRRAHLRLCLERLKTLP 104

FIG. 3